

SEQUENCE LISTING

(1) GENERAL INFORMATION

- (i) APPLICANT: Goli, Surya K.
Hillman, Jennifer L.
- (ii) TITLE OF THE INVENTION: A NOVEL GLUTATHIONE S-TRANSFERASE
- (iii) NUMBER OF SEQUENCES: 5
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: INCYTE GENOMICS, INC.
 - (B) STREET: 3160 Porter Drive
 - (C) CITY: Palo Alto
 - (D) STATE: CA
 - (E) COUNTRY: US
 - (F) ZIP: 94304
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Diskette
 - (B) COMPUTER: IBM Compatible
 - (C) OPERATING SYSTEM: DOS
 - (D) SOFTWARE: FastSEQ
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: 09/309,320
 - (B) FILING DATE: May 11, 1999
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: 09/309,320
 - (B) FILING DATE: May 11, 1999
 - (A) APPLICATION NUMBER: 09/096,571
 - (B) FILING DATE: June 12, 1998
 - (A) APPLICATION NUMBER: 08/756,771
 - (B) FILING DATE: November 26, 1996
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Billings, Lucy J.
 - (B) REGISTRATION NUMBER: 36,749
 - (C) REFERENCE/DOCKET NUMBER: PF-0162 US
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: 415-855-0555
 - (B) TELEFAX: 415-845-4166
 - (C) TELEX:

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 222 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: Consensus
(B) CLONE: Consensus

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

```

Met Ala Ala Arg Pro Lys Leu His Tyr Pro Asn Gly Arg Gly Arg Met
 1           5           10           15
Glu Ser Val Arg Trp Val Leu Ala Ala Ala Gly Val Glu Phe Asp Glu
 20           25           30
Glu Phe Leu Glu Thr Lys Glu Gln Leu Tyr Lys Leu Gln Asp Gly Asn
 35           40           45
His Leu Leu Phe Gln Gln Val Pro Met Val Glu Ile Asp Gly Met Lys
 50           55           60
Leu Val Gln Thr Arg Ser Ile Leu His Tyr Ile Ala Asp Lys His Asn
 65           70           75           80
Leu Phe Gly Lys Asn Leu Lys Glu Arg Thr Leu Ile Asp Met Tyr Val
 85           90           95
Glu Gly Thr Leu Asp Leu Leu Glu Leu Leu Ile Met His Pro Phe Leu
100           105           110
Lys Pro Asp Asp Gln Gln Lys Glu Val Val Asn Met Ala Gln Lys Ala
115           120           125
Ile Ile Arg Tyr Phe Pro Val Phe Glu Lys Ile Leu Arg Gly His Gly
130           135           140
Gln Ser Phe Leu Val Gly Asn Gln Leu Ser Leu Ala Asp Val Ile Leu
145           150           155           160
Leu Gln Thr Ile Leu Ala Leu Glu Glu Lys Ile Pro Asn Ile Leu Ser
165           170           175
Ala Phe Pro Phe Leu Gln Glu Tyr Thr Val Lys Leu Ser Asn Ile Pro
180           185           190
Thr Ile Lys Arg Phe Leu Glu Pro Gly Ser Lys Lys Lys Pro Pro Pro
195           200           205
Asp Glu Ile Tyr Val Arg Thr Val Tyr Asn Ile Phe Arg Pro
210           215           220

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(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 800 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: Consensus
(B) CLONE: Consensus

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

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ATGGCAGCAA GGCCCAAGCT CCACTATCCC AACGGAAGAG GCCGGATGGA GTCCGTGAGA      60
TGGGTTTTAG CTGCCGCCGG AGTCGAGTTT GATGAAGAAT TTCTGGAAC AAAAGAACAG      120
TTGTACAAGT TGCAGGATGG TAACCACCTG CTGTTCCAAC AAGTGCCCAT GGTGAAATT      180
GACGGGATGA AGTTGGTACA GACCCGAAGC ATTCTCCACT ACATAGCAGA CAAGCACAAT      240
CTCTTTGGCA AGAACCTCAA GGAGAGAACC CTGATTGACA TGTACGTGGA GGGGACACTG      300
GATCTGCTGG AACTGCTTAT CATGCATCCT TTCTTAAAC CAGATGATCA GCAAAAGGAA      360
GTGGTTAACA TGGCCCAGAA GGCTATAATT AGATACTTTC CTGTGTTTGA AAAGATTTTA      420
AGGGGTCACG GACAAAGCTT TCTTGTTGGT AATCAGCTGA GCCTTGCGA TGTGATTTTA      480
CTCAAACCA TTTTAGCTCT AGAAGAGAAA ATTCCTAATA TCCTGTCTGC ATTCCTTTC      540
CTCCAGGAAT ACACAGTGAA ACTAAGTAAT ATCCCTACAA TTAAGAGATT CCTTGAACCT      600
GGCAGCAAGA AGAAGCCTCC CCTGATGAA ATTTATGTGA GAACCGTCTA CAACATCTTT      660
AGGCCATAAA ACAACACATC CATGTGTGAG TGACAGTGTG TTCCTAGAGA TGGTATTGTC      720

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TACAGTCATG TCTTAATGGA TCCCAGCTCT GTCATGGTGC TATCTATGTA TTAAGTTGGG 780
 TCCTAAGTTG GGTCTTTTGT 800

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 222 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: GenBank
- (B) CLONE: 825605

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Glu | Lys | Pro | Lys | Leu | His | Tyr | Ser | Asn | Thr | Arg | Gly | Arg | Met |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |
| Glu | Ser | Ile | Arg | Trp | Leu | Leu | Ala | Ala | Gly | Val | Glu | Phe | Glu | Glu | |
| | | | 20 | | | | | 25 | | | | | 30 | | |
| Lys | Phe | Ile | Lys | Ser | Ala | Glu | Asp | Leu | Asp | Lys | Leu | Arg | Asn | Asp | Gly |
| | | | 35 | | | | 40 | | | | | 45 | | | |
| Tyr | Leu | Met | Phe | Gln | Gln | Val | Pro | Met | Val | Glu | Ile | Asp | Gly | Met | Lys |
| | 50 | | | | | 55 | | | | | 60 | | | | |
| Leu | Val | Gln | Thr | Arg | Ala | Ile | Leu | Asn | Tyr | Ile | Ala | Ser | Lys | Tyr | Asn |
| 65 | | | | | 70 | | | | | 75 | | | | | 80 |
| Leu | Tyr | Gly | Lys | Asp | Ile | Lys | Glu | Lys | Ala | Leu | Ile | Asp | Met | Tyr | Ile |
| | | | 85 | | | | | 90 | | | | | 95 | | |
| Glu | Gly | Ile | Ala | Asp | Leu | Gly | Glu | Met | Ile | Leu | Leu | Leu | Pro | Phe | Thr |
| | | | 100 | | | | | 105 | | | | | 110 | | |
| Gln | Pro | Glu | Glu | Gln | Asp | Ala | Lys | Leu | Ala | Leu | Ile | Gln | Glu | Lys | Thr |
| | | | 115 | | | | 120 | | | | | | 125 | | |
| Lys | Asn | Arg | Tyr | Phe | Pro | Ala | Phe | Glu | Lys | Val | Leu | Lys | Ser | His | Gly |
| | 130 | | | | | 135 | | | | | 140 | | | | |
| Gln | Asp | Tyr | Leu | Val | Gly | Asn | Lys | Leu | Ser | Arg | Ala | Asp | Ile | His | Leu |
| 145 | | | | | 150 | | | | | 155 | | | | | 160 |
| Val | Glu | Leu | Leu | Tyr | Tyr | Val | Glu | Glu | Leu | Asp | Ser | Ser | Leu | Ile | Ser |
| | | | 165 | | | | | | 170 | | | | | 175 | |
| Ser | Phe | Pro | Leu | Leu | Lys | Ala | Leu | Lys | Thr | Arg | Ile | Ser | Asn | Leu | Pro |
| | | | 180 | | | | | 185 | | | | | 190 | | |
| Thr | Val | Lys | Lys | Phe | Leu | Gln | Pro | Gly | Ser | Pro | Arg | Lys | Pro | Pro | Met |
| | | 195 | | | | 200 | | | | | | 205 | | | |
| Asp | Glu | Lys | Ser | Leu | Glu | Glu | Ser | Arg | Lys | Ile | Phe | Arg | Phe | | |
| 210 | | | | | | 215 | | | | | | 220 | | | |

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 222 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: GenBank
- (B) CLONE: 259141

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Ala Glu Lys Pro Lys Leu His Tyr Phe Asn Ala Arg Gly Arg Met

| | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| 1 | | | | 5 | | | | | 10 | | | | | 15 | | | |
| Glu | Ser | Thr | Arg | Trp | Leu | Leu | Ala | Ala | Ala | Gly | Val | Glu | Phe | Glu | Glu | | |
| | | | 20 | | | | | 25 | | | | | 30 | | | | |
| Lys | Phe | Ile | Lys | Ser | Ala | Glu | Asp | Leu | Asp | Lys | Leu | Arg | Asn | Asp | Gly | | |
| | | 35 | | | | | 40 | | | | | 45 | | | | | |
| Tyr | Leu | Met | Phe | Gln | Gln | Val | Pro | Met | Val | Glu | Ile | Ala | Ser | Lys | Tyr | Asn | |
| | 50 | | | | | 55 | | | | | 60 | | | | | | |
| Leu | Val | Gln | Thr | Arg | Ala | Ile | Leu | Asn | Tyr | Ile | Ala | Ser | Lys | Tyr | Asn | | |
| 65 | | | | | 70 | | | | | 75 | | | | | 80 | | |
| Leu | Tyr | Gly | Lys | Asp | Ile | Lys | Glu | Arg | Ala | Leu | Ile | Asp | Met | Tyr | Ile | | |
| | | | 85 | | | | | | 90 | | | | | 95 | | | |
| Glu | Gly | Ile | Ala | Asp | Leu | Gly | Glu | Met | Ile | Leu | Leu | Leu | Pro | Val | Cys | | |
| | | | 100 | | | | | 105 | | | | | 110 | | | | |
| Pro | Pro | Glu | Glu | Lys | Asp | Ala | Lys | Leu | Ala | Leu | Ile | Lys | Glu | Lys | Ile | | |
| | | 115 | | | | | 120 | | | | | 125 | | | | | |
| Lys | Asn | Arg | Tyr | Phe | Pro | Ala | Phe | Glu | Lys | Val | Leu | Lys | Ser | His | Gly | | |
| | 130 | | | | | 135 | | | | | 140 | | | | | | |
| Gln | Asp | Tyr | Leu | Val | Gly | Asn | Lys | Leu | Ser | Arg | Ala | Asp | Ile | His | Leu | | |
| 145 | | | | | 150 | | | | | 155 | | | | | 160 | | |
| Val | Glu | Leu | Leu | Tyr | Tyr | Val | Glu | Glu | Leu | Asp | Ser | Ser | Leu | Ile | Ser | | |
| | | | 165 | | | | | | 170 | | | | | 175 | | | |
| Ser | Phe | Pro | Leu | Leu | Lys | Ala | Leu | Lys | Thr | Arg | Ile | Ser | Asn | Leu | Pro | | |
| | | 180 | | | | | | 185 | | | | | 190 | | | | |
| Thr | Val | Lys | Lys | Phe | Leu | Gln | Pro | Gly | Ser | Pro | Arg | Lys | Pro | Pro | Met | | |
| | 195 | | | | | 200 | | | | | | 205 | | | | | |
| Asp | Glu | Lys | Ser | Leu | Glu | Glu | Ala | Arg | Lys | Ile | Phe | Arg | Phe | | | | |
| | 210 | | | | | 215 | | | | | 220 | | | | | | |

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 222 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: GenBank
- (B) CLONE: 193710

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

| | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Ala | Ala | Lys | Pro | Lys | Leu | Tyr | Tyr | Phe | Asn | Gly | Arg | Gly | Arg | Met | | |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | | | |
| Glu | Ser | Ile | Arg | Trp | Leu | Leu | Ala | Ala | Ala | Gly | Val | Glu | Phe | Glu | Glu | | |
| | | | 20 | | | | | 25 | | | | | 30 | | | | |
| Glu | Phe | Leu | Glu | Thr | Arg | Glu | Gln | Tyr | Glu | Lys | Met | Gln | Lys | Asp | Gly | | |
| | | 35 | | | | | 40 | | | | | 45 | | | | | |
| His | Leu | Leu | Phe | Gly | Gln | Val | Pro | Leu | Val | Glu | Ile | Ala | Ala | Lys | Tyr | Asn | |
| | 50 | | | | | 55 | | | | | 60 | | | | | | |
| Leu | Thr | Gln | Thr | Arg | Ala | Ile | Leu | Ser | Tyr | Leu | Ala | Ala | Lys | Tyr | Asn | | |
| 65 | | | | | 70 | | | | | 75 | | | | | 80 | | |
| Leu | Tyr | Gly | Lys | Asp | Leu | Lys | Glu | Arg | Val | Arg | Ile | Asp | Met | Tyr | Ala | | |
| | | | 85 | | | | | | 90 | | | | | 95 | | | |
| Asp | Gly | Thr | Gln | Asp | Leu | Met | Met | Met | Ile | Ala | Val | Ala | Pro | Phe | Lys | | |
| | | 100 | | | | | | 105 | | | | | 110 | | | | |
| Thr | Pro | Lys | Glu | Lys | Glu | Glu | Ser | Tyr | Asp | Leu | Ile | Leu | Ser | Arg | Ala | | |
| | 115 | | | | | | 120 | | | | | 125 | | | | | |
| Lys | Thr | Arg | Tyr | Phe | Pro | Val | Phe | Glu | Lys | Ile | Leu | Lys | Asp | His | Gly | | |
| | 130 | | | | | 135 | | | | | 140 | | | | | | |
| Glu | Ala | Phe | Leu | Val | Gly | Asn | Gln | Leu | Ser | Trp | Ala | Asp | Ile | Gln | Leu | | |

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| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 145 | | | | | 150 | | | | | 155 | | | | 160 | |
| Leu | Glu | Ala | Ile | Leu | Met | Val | Glu | Glu | Leu | Ser | Ala | Pro | Val | Leu | Ser |
| | | | | 165 | | | | | 170 | | | | | 175 | |
| Asp | Phe | Pro | Leu | Leu | Gln | Ala | Phe | Lys | Thr | Arg | Ile | Ser | Asn | Ile | Pro |
| | | | 180 | | | | | 185 | | | | | 190 | | |
| Thr | Ile | Lys | Lys | Phe | Leu | Gln | Pro | Gly | Ser | Gln | Arg | Lys | Pro | Pro | Pro |
| | | 195 | | | | | 200 | | | | | 205 | | | |
| Asp | Gly | Pro | Tyr | Val | Glu | Val | Val | Arg | Ile | Val | Leu | Lys | Phe | | |
| | 210 | | | | | 215 | | | | | 220 | | | | |